

# Patent Screen Results

Your Fasta Input (protein sequence):

>CL001165, SEQ ID NO:2, July 22, 2003

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501 FQESNSLRPV ACRHCKALIL GIYKQGLKCR ACGVNCHKQC KDRLSVECCR
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601 EEVQTVEDGV FDIHL

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BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001165, SEQ ID NO:2, July 22, 2003  
(615 letters)

Database: /work/eda3/blast/public/geneseqp\_all.fasta  
952,616 sequences; 143,563,330 total letters

Sequences producing significant alignments:	Score (bits)	E Value
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 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480  
 Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC  
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
 Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPLAEIRE 600  
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE  
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 594  
 Query: 601 EEVQTVEDGVFDIHL 615  
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 Sbjct: 595 EEVQTVEDGVFDIHL 609

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Score = 1241 bits (3176), Expect = 0.0  
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60  
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 Sbjct: 120 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 179  
 Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 120  
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID  
 Sbjct: 180 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPALAEQIKELKALLDQEGNRRHSSLID 239  
 Query: 121 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180  
 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS  
 Sbjct: 240 IDSVPTYKWKQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 299  
 Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 240  
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF  
 Sbjct: 300 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 359  
 Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300  
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR  
 Sbjct: 360 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 419  
 Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360  
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL  
 Sbjct: 420 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 479

Query: 361 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420  
 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ  
 Sbjct: 480 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 539

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480  
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM  
 Sbjct: 540 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 599

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC  
 Sbjct: 600 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 659

Query: 541 KDRLSVECRRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPAEIRE 600  
 KDRLSVECRRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE  
 Sbjct: 660 KDRLSVECRRRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 713

Query: 601 EEVQTVEDGVFDIHL 615  
 EEVQTVEDGVFDIHL  
 Sbjct: 714 EEVQTVEDGVFDIHL 728

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Score = 1241 bits (3176), Expect = 0.0  
 Identities = 608/615 (98%), Positives = 609/615 (98%), Gaps = 6/615 (0%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60  
 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLAAKLLHIY  
 Sbjct: 56 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLAAKLLHIY 115

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120  
 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID  
 Sbjct: 116 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 175

Query: 121 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180  
 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS  
 Sbjct: 176 IDSVPTYKWKQRQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 235

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 240  
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF  
 Sbjct: 236 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 295

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300  
 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR  
 Sbjct: 296 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 355

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360  
 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL  
 Sbjct: 356 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 415

Query: 361 LSLTLVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420

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Query:	421	A	L	V	V	E	H	I	E	K	M	V	E	S	V	F	R	N	F	D	V	D	G	D	G	H	I	S	Q	E	E	F	Q	I	I	R	G	N	F	P	Y	L	S	A	F	G	D	L	D	Q	N	Q	D	G	C	I	S	R	E	E	M	480
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Sbjct:	476	A	L	V	V	E	H	I	E	K	M	V	E	S	V	F	R	N	F	D	V	D	G	D	G	H	I	S	Q	E	E	F	Q	I	I	R	G	N	F	P	Y	L	S	A	F	G	D	L	D	Q	N	Q	D	G	C	I	S	R	E	E	M	535
Query:	481	V	S	Y	F	L	R	S	S	S	V	L	G	G	R	M	G	F	V	H	N	F	Q	E	S	N	S	L	R	P	V	A	C	R	H	C	K	A	L	I	L	G	I	Y	K	Q	G	L	K	R	A	C	G	V	N	C	H	K	Q	540		
		V	S	Y	F	L	R	S	S	S	V	L	G	G	R	M	G	F	V	H	N	F	Q	E	S	N	S	L	R	P	V	A	C	R	H	C	K	A	L	I	L	G	I	Y	K	Q	G	L	K	R	A	C	G	V	N	C	H	K	Q			
Sbjct:	536	V	S	Y	F	L	R	S	S	S	V	L	G	G	R	M	G	F	V	H	N	F	Q	E	S	N	S	L	R	P	V	A	C	R	H	C	K	A	L	I	L	G	I	Y	K	Q	G	L	K	R	A	C	G	V	N	C	H	K	Q	595		
Query:	541	K	D	R	L	S	V	E	C	R	R	R	A	Q	S	V	S	L	E	G	S	A	P	S	P	S	P	M	H	S	H	H	R	A	F	S	F	S	L	P	R	P	G	R	R	G	S	R	P	P	A	I	P	L	P	A	E	I	R	E	600	
		K	D	R	L	S	V	E	C	R	R	R	A	Q	S	V	S	L	E	G	S	A	P	S	P	S	P	M	H	S	H	H	R	A	F	S	F	S	L	P	R	P	G	R	R	G	S	R	P	P	E	I	R	E								
Sbjct:	596	K	D	R	L	S	V	E	C	R	R	R	A	Q	S	V	S	L	E	G	S	A	P	S	P	S	P	M	H	S	H	H	R	A	F	S	F	S	L	P	R	P	G	R	R	G	S	R	P	P	-----	E	I	R	E	649						
Query:	601	E	E	V	Q	T	V	E	D	G	V	F	D	I	H	L	615																																													
		E	E	V	Q	T	V	E	D	G	V	F	D	I	H	L																																														
Sbjct:	650	E	E	V	Q	T	V	E	D	G	V	F	D	I	H	L	664																																													



Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480  
 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM  
 Sbjct: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC  
 Sbjct: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPPAIPPAEIRE 600  
 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP EIRE  
 Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHSHHHRAFSFSLPRPGRRGSRPP-----EIRE 594

Query: 601 EEVQTVEDGVFDIHL 615  
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 Length = 608

Score = 1202 bits (3076), Expect = 0.0  
 Identities = 589/615 (95%), Positives = 597/615 (96%), Gaps = 7/615 (1%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60  
 MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y  
 Sbjct: 1 MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLH FY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNP ELAEQIKELKALLDQEGNRRHSSLID 120  
 QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNP ELAE IKELKALLDQEGNRRHSSLID  
 Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWVSAPPAEFDLNP ELAEPIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPTYKWK RQVTQRNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180  
 I+SVPTYKWK RQVTQRNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS  
 Sbjct: 121 IESVPTYKWK RQVTQRNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQ RALVITHFVHVAEKLLQLQNF 240  
 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA Q RALVITHFVHVAEKLLQLQNF  
 Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQ RALVITHFVHVAEKLLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGN YRRRLAACVGFR 300  
 NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR  
 Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLD PARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360  
 FPILGVHLKDLVALQLALPDWLD P RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL  
 Sbjct: 301 FPILGVHLKDLVALQLALPDWLD PGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360

Query: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAAKPKLDQ 420  
 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAKPKLDQ  
 Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTSCTPPPRPPVLEEWTSAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNQDGCISREEM 480

ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM  
Sbjct: 421 ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
+SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC  
Sbjct: 481 ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHRAFSFSLPRPGRGSRPPAIPLP AEIRE 600  
KDRLSVECRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP EIRE  
Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSP THT-HHRAFSFSLPRPGRRSSRPP-----EIRE 593

Query: 601 EEVQTVEDGVFDIHL 615  
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Length = 608

Score = 1202 bits (3076), Expect = 0.0  
Identities = 589/615 (96%), Positives = 597/615 (96%), Gaps = 7/615 (1%)

Query: 1 MAGTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRIFLMMHPWYIPSSQLAAKLLHIY 60  
MA TLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVR+FLMMHPWYIPSSQLA+KLLH Y  
Sbjct: 1 MASTLDLDKGCTVEELLRGCIEAFDDSGKVRDPQLVRMFLMMHPWYIPSSQLASKLLH FY 60

Query: 61 QQSRKDNSNSLQVKTCHLVRYWISAFPAEFDLNPELAEQIKELKALLDQEGNRRHSSLID 120  
QQSRKDNSNSLQVKTCHLVRYW+SAFPAEFDLNPELAE IKELKALLDQEGNRRHSSLID  
Sbjct: 61 QQSRKDNSNSLQVKTCHLVRYWVSAPPAEFDLNPELAEPIKELKALLDQEGNRRHSSLID 120

Query: 121 IDSVPTYKWKQVTRQNPVGQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180  
I+SVPTYKWKQVTRQNPV QKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS  
Sbjct: 121 IESVPTYKWKQVTRQNPVEQKKRKMSLLFDHLEPMELAEHLTYLEYRSFCKILFQDYHS 180

Query: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTAPQRALVITHFVHVAEKLQLQNF 240  
FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTA QRALVITHFVHVAEKLQLQNF  
Sbjct: 181 FVTHGCTVDNPVLERFISLFNSVSQWVQLMILSKPTATQRALVITHFVHVAEKLQLQNF 240

Query: 241 NTLMAVVGGLSHSSISRLKETHSHVSPETIKLWEGLTELVTATGNYGNRRRLAACVGFR 300  
NTLMAVVGGLSHSSISRLKETHSHVSP+TIKLWEGLTELVTATGNY NYRRRLAACVGFR  
Sbjct: 241 NTLMAVVGGLSHSSISRLKETHSHVSPDTIKLWEGLTELVTATGNYSNYRRRLAACVGFR 300

Query: 301 FPILGVHLKDLVALQLALPDWLDPARTRLNGAKMKQLFSILEELAMVTSLRPPVQANPDL 360  
FPILGVHLKDLVALQLALPDWLDP RTRLNGAKM+QLFSILEELAMVTSLRPPVQANPDL  
Sbjct: 301 FPILGVHLKDLVALQLALPDWLDPGRTRLNGAKMRQLFSILEELAMVTSLRPPVQANPDL 360

Query: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTSAAKPKLDQ 420  
LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTS AKPKLDQ  
Sbjct: 361 LSLLTVSLDQYQTEDELYQLSLQREPRSKSSPTSPTCTPPPRPPVLEEWTSVAKPKLDQ 420

Query: 421 ALVVEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480  
ALV EHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM  
Sbjct: 421 ALVAEHIEKMVESVFRNFDVDGDGHISQEEFQIIRGNFPYLSAFGDLDQNDGCISREEM 480

Query: 481 VSYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540  
+SYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC  
Sbjct: 481 ISYFLRSSSVLGGRMGFVHNFQESNSLRPVACRHCKALILGIYKQGLKCRACGVNCHKQC 540

Query: 541 KDRLSVECRRAQSVSLEGSAPSPSPMHHRAFSFSLPRPGRRGSRPPAIPPLPAEIRE 600  
KDRLSVECRRAQSVSLEGSAPSPSP H+ HHRAFSFSLPRPGRR SRPP EIRE  
Sbjct: 541 KDRLSVECRRAQSVSLEGSAPSPSPHTT-HHRAFSFSLPRPGRRSSRPP-----EIRE 593

Query: 601 EEVQTVEDGVFDIHL 615  
EEVQTVEDGVFDIHL  
Sbjct: 594 EEVQTVEDGVFDIHL 608

Database: /work/eda3/blast/public/geneseqp\_all.fasta  
Posted date: Mar 2, 2003 3:26 AM  
Number of letters in database: 143,563,330  
Number of sequences in database: 952,616

Lambda	K	H
0.321	0.136	0.410

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 185709453  
Number of Sequences: 952616  
Number of extensions: 7789331  
Number of successful extensions: 34968  
Number of sequences better than 1.0e-08: 106  
Number of HSP's better than 0.0 without gapping: 58  
Number of HSP's successfully gapped in prelim test: 48  
Number of HSP's that attempted gapping in prelim test: 34702  
Number of HSP's gapped (non-prelim): 171  
length of query: 615  
length of database: 143,563,330  
effective HSP length: 55  
effective length of query: 560  
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effective search space: 51054892000  
effective search space used: 51054892000  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.8 bits)  
X3: 64 (24.9 bits)  
S1: 41 (21.9 bits)  
S2: 149 (62.5 bits)